Soohyun Lee

List of Publications by Year
in descending order

32 papers	6,065 citations	279798 23 h-index	414414 32 g-index
39 all docs	39 docs citations	39 times ranked	9702 citing authors

#	Article	IF	Citations
1	Hi-C Data Formats. Methods in Molecular Biology, 2022, 2301, 133-141.	0.9	0
2	Pairs and Pairix: a file format and a tool for efficient storage and retrieval for Hi-C read pairs. Bioinformatics, 2022, 38, 1729-1731.	4.1	7
3	The 4D Nucleome Data Portal as a resource for searching and visualizing curated nucleomics data. Nature Communications, 2022, 13, 2365.	12.8	49
4	HiTea: a computational pipeline to identify non-reference transposable element insertions in Hi-C data. Bioinformatics, 2021, 37, 1045-1051.	4.1	3
5	BamSnap: a lightweight viewer for sequencing reads in BAM files. Bioinformatics, 2021, 37, 263-264.	4.1	5
6	Sustainable data analysis with Snakemake. F1000Research, 2021, 10, 33.	1.6	188
7	Sustainable data analysis with Snakemake. F1000Research, 2021, 10, 33.	1.6	642
8	Comprehensive identification of transposable element insertions using multiple sequencing technologies. Nature Communications, 2021, 12, 3836.	12.8	44
9	Whole-genome analysis reveals the contribution of non-coding de novo transposon insertions to autism spectrum disorder. Mobile DNA, 2021, 12, 28.	3.6	17
10	HiNT: a computational method for detecting copy number variations and translocations from Hi-C data. Genome Biology, 2020, 21, 73.	8.8	56
11	Tibanna: software for scalable execution of portable pipelines on the cloud. Bioinformatics, 2019, 35, 4424-4426.	4.1	11
12	HiGlass: web-based visual exploration and analysis of genome interaction maps. Genome Biology, 2018, 19, 125.	8.8	950
13	Linking transcriptional and genetic tumor heterogeneity through allele analysis of single-cell RNA-seq data. Genome Research, 2018, 28, 1217-1227.	5.5	172
14	DUSP9 Modulates DNA Hypomethylation in Female Mouse Pluripotent Stem Cells. Cell Stem Cell, 2017, 20, 706-719.e7.	11.1	63
15	NGSCheckMate: software for validating sample identity in next-generation sequencing studies within and across data types. Nucleic Acids Research, 2017, 45, e103-e103.	14.5	95
16	Analyzing Somatic Genome Rearrangements in Human Cancers by Using Whole-Exome Sequencing. American Journal of Human Genetics, 2016, 98, 843-856.	6.2	33
17	EMSAR: estimation of transcript abundance from RNA-seq data by mappability-based segmentation and reclustering. BMC Bioinformatics, 2015, 16, 278.	2.6	18
18	Somatic mutation in single human neurons tracks developmental and transcriptional history. Science, 2015, 350, 94-98.	12.6	486

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19	Failure to replicate the STAP cell phenomenon. Nature, 2015, 525, E6-E9.	27.8	41
20	Hallmarks of pluripotency. Nature, 2015, 525, 469-478.	27.8	338
21	A comparison of genetically matched cell lines reveals the equivalence of human iPSCs and ESCs. Nature Biotechnology, 2015, 33, 1173-1181.	17.5	235
22	Comparative analysis of metazoan chromatin organization. Nature, 2014, 512, 449-452.	27.8	363
23	Global mapping of translation initiation sites in mammalian cells at single-nucleotide resolution. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E2424-32.	7.1	534
24	Accurate quantification of transcriptome from RNA-Seq data by effective length normalization. Nucleic Acids Research, 2011, 39, e9-e9.	14.5	101
25	Relative Codon Adaptation Index, a Sensitive Measure of Codon Usage Bias. Evolutionary Bioinformatics, 2010, 6, EBO.S4608.	1.2	46
26	Collapse of Germline piRNAs in the Absence of Argonaute3 Reveals Somatic piRNAs in Flies. Cell, 2009, 137, 509-521.	28.9	503
27	The Drosophila HP1 Homolog Rhino Is Required for Transposon Silencing and piRNA Production by Dual-Strand Clusters. Cell, 2009, 138, 1137-1149.	28.9	382
28	Endogenous siRNAs Derived from Transposons and mRNAs in *Drosophila* Somatic Cells. Science, 2008, 320, 1077-1081.	12.6	594
29	Quantitative Analysis of Single Nucleotide Polymorphisms within Copy Number Variation. PLoS ONE, 2008, 3, e3906.	2.5	34
30	The complete genome sequence of a dog: a perspective. BioEssays, 2006, 28, 569-573.	2.5	3
31	Genes involved in complex adaptive processes tend to have highly conserved upstream regions in mammalian genomes. BMC Genomics, 2005, 6, 168.	2.8	26
32	CHOISS for selection of single nucleotide polymorphism markers on interval regularity. Bioinformatics, 2004, 20, 581-582.	4.1	4